

Percent Similarity: 38.83% Conservative: 23
 Best Local Similarity: 25.60% Mismatches: 66
 Query Match: 8.91% Indels: 50
 DB: 1 Gaps: 8

US-09-252-991A-26292 (1-245) x US-09-252-991A-5802 (1-735)

Qy 3 ThrSerThrCysGlyAlaIleProArgProValGlyLysThrGlyAlaAlaGlyArgAla 22

Db 43 TCACTCTCTCTGTCATGCCTCGCTCCCTCCACGCTCTTACAG----- 90

Qy 23 AspGluArgHisArgAlaAlaAlaAspAspProGluLysGlyTrpSerAlaLeuAspAspGln 42

Db 91 -----CGGCCAACCCACCCACCGGACCCGCCTCCATGCCGATGCCACCCGAGAC 144

Qy 43 LysAlaArgGluValIleLeuGluIleValIleArgGlyGlnLeuThrAspProGluSer 62

Db 145 CCTGCCGCCCA-----CGCGCAGCCAGCTGCAG 177

Qy 63 AlaArg---GlyLysIleLeuGluThrAlaAlaHisLeuPheArgSerLysGlyTrpGlu 81

Db 178 GTCGCGTCGAGGAGCTGATGCCGGGGCGAGCAACTGTTCTAGACAAGGGTGCGGAC 237

Qy 82 ArgThrThrValArgAspLeuAlaSerAlaValGlyTleGinSerGlySerTlePheHis 101

Db 238 GCAACACCATGAGGACATCCCTCCGCGGGGCGCCAGGTACCTCTATCAC 297

Qy 102 HisPheLysSerLysAspGluIleLeuArgSerValMetGluGlu---ThrIleLeuThr 120

Db 298 TACTTCAAGCCAGGCCACTCCCTGGCTACGGCTTACGCCAGCTTCACCCAGGCTTC 357

Qy 121 AspThrAlaLeuMetArgAlaAlaLeuAla---AspAlaGluAspLeu----- 135

Db 358 CAGCAGCGCATGCCGAATGCCGCTGCCGGCAGGACCA-TCCGGCCGCT 416

Qy 136 -----ArgGluArgValLeuGlyIleLeu-----IleArgCys 145

Db 417 GCGCGCTGGAGCGAGGGCTTGAGGGCTACGGCTCACGGCTCACGATG 476

Qy 146 GluLeuGin----- 148

Db 477 GGCTCTAGAGCGGACCATCACGACCAACCGAGGCGGACCGGGTGTGGA 536

Qy 149 SerIleMetGlyGlyIleGlyGlu 156

Db 537 GCAATTGGGGAGCTACTGGAGAA 560

Qy RESULT 15

US-09-252-991A-7944

Sequence 7944, Application US/09252991A

Patient No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7944

LENGTH: 576

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7944

Alignment Scores:

Pred. No.: 0.179

Score: 111.00

Percent Similarity: 44.16%

Best Local Similarity: 27.7% Mismatches: 68
 Query Match: 8.87% Indels: 18
 DB: 1 Gaps: 6

US-09-252-991A-26292 (1-245) x US-09-252-991A-7944 (1-576)

Qy 60 ProGluSerAlaArg-----GlyLysIleLeuGluThrAlaAlaHisLeu 74

Db 38 CGCAGAGGCCGTCACCGCAGTTGGTGGCGAGCACCTCGAGGCGCCTTCAGGTT 97

Qy 75 PheArgSerLysGlyTrpGluArgThrValArgAspLeuAlaSerAlaValGlyIle 94

Db 98 CGGCCAGCGGAGGCGCAAGGTTTACCCACGCCGGGCGGCCGG 157

Qy 95 GlnSerGlySerTlePheHisLsPhoIysSerLysAspGluIleLeuArgSerValMet 114

Db 158 AGCATCGGTTGCCGTCAGCAGTATTCGGAAACAAGGGGGATCTCTCCGCCCTGCAA 217

Qy 115 GluGluIleLeuLeuThrAlaLeuMetArgAlaAlaLeuAlaAspAla----- 132

Db 218 AGCGACGGTGGGGCGACACGGCTTCGAGACACGCCGG 277

Qy 133 -----GluAspLeuArgGluArgValLeuGlyIleLeuArg-----CysGluLeu 147

Db 338 GCGCGATACGGCTGGCCCTGAGCAGCCGGCCGGCTGATCGCGAGGCCGACGCCG 397

Qy 166 ArgSerIleLeuAspAlaGluGlu-----GlnAlaIleLeuAspAspIleTyrGlu 184

Db 398 CGGGAGGGAAGGGAGGGCGGCCGGTGTGTCAGGGTTCCTCCGGAGGCCCTGGCC 457

Qy 185 GlnMetTripleAspValLeuGlyIleLeuAlaArgLeuAlaGly 198

Db 458 GAGGT-----GCGAGGCCGAGGCCGCTGGCCGC 490

Search completed: April 29, 2003, 16:15:09
 Job time : 5087 secs

; APPLICANT: MARC J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/094,190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 9166
 ; LENGTH: 423
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-9166

Alignment Scores:
 Pred. No.: 0.0709
 Score: 113.50
 Percent Similarity: 36.65%
 Best Local Similarity: 22.36%
 Query Match: 9.07%
 DB: 1

Length: 423
 Matches: 36
 Conservative: 23
 Mismatches: 57
 Indels: 46
 Gaps: 3

US-09-252-991A-26292 (1-245) x US-09-252-991A-9166 (1-423)

QY 44 AlaArgGluValMetLeuGluLeuValAlaThrGlyGlnLeuThrPrgluserAla 63
 Db 384 GCCCCGCAAGCTCTGGCCGAGATGATC-----GAGGAACC 349

QY 64 ArgGlyLysLeuLeuGlnThrAlaAlaAlaHisLeuPheArgSerLysGlyTyrGluArgThr 83
 Db 348 CGCGGCAAGCTGATGCGACGCCGCCGCCGAGCTGCGGACACGGCTAGCCGCCGCC 289

QY 84 ThrValLargAspLeuAlaSerAlaValAlaGlyLeuGinSerGlySerIlePheHisIlePhe 103
 Db 288 TCGATGTCGACACTGACGCCAGGCCGCTCACCGCCGAGCCGCTGATCACCTC 229

QY 104 LysSerLysAspGluIleLeuArgSerValMetGluGluThrIleLeuIleuIleuIleu 123
 Db 228 GGGGACAAGAGAACGGCTGCTGGCCGGTGGCAAGCAGACGAGGATGATCTT 169

QY 124 LeuMetArgAlaAlaLeuAlaAspAlaGluAspLeuArgGluAlaValGluLeu 143
 Db 168 CGCCCTGGCCCATCTGGCTGGCCGGCAGGACCTC-----133

QY 144 ArgGlyGluLeuGinSerIleMetGlyGlyGlyGluAlaMetAlaValAlaLeu 163
 Db 133 -----133

QY 164 GlutpArgSerLeuSerAlaIleGluGlyGlnAlaIleArgIleLeuGlyLeuArgAspIleTyr 183
 Db 132 - -TGGAGGGGCTTCGGCTACACCGGGCTACTG-----97

QY 184 GluGlnMetTripleAspValLeuGlyGluAlaArgLeuAlaGlyTyrGlyGlyAsp 203
 Db 96 - -GAATGGCCCTGGAAAGCGGA-AATCCAGCGCATGRCCTGGCGATGCCGGCCAT 41

QY 204 Pro 204
 Db 40 CCT 38

RESULT 11
 US-09-252-991A-1993
 ; Sequence 1993, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/094,190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 9166
 ; LENGTH: 654
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1993

Alignment Scores:
 Pred. No.: 0.1446
 Score: 113.50
 Percent Similarity: 50.98%
 Best Local Similarity: 34.31%
 Query Match: 9.07%
 DB: 1

Length: 654
 Matches: 35
 Conservative: 17
 Mismatches: 27
 Indels: 23
 Gaps: 4

US-09-252-991A-26292 (1-245) x US-09-252-991A-1993 (1-654)

QY 66 LysLeuGluGinThrAlaAlaAlaHisLeuPheArgSerLysGlyTyrGluArgThrVal 85
 Db 64 GAGATCTTCGATACCCCTCAAGCAGTTCTCGAACAGGGAGAACACGTAACGGTC 123

QY 86 ArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHisIlePheHisSer 105
 Db 124 GAGATGATCGGGATGCCGTCGGCATGGCAAGGCAGATCTACAGCACTTCAGTCC 183

QY 106 LysAspGluIleLeuArgSerValMetGluGluThrIleLeuTyrAsnThrAlaLeuMet 125
 Db 184 AAGGGGAGATCTACTGTCGCCGCTGATGCTGAG 231

QY 126 ArgAlaAlaLeuAlaAspAlaGluAspLeu---ArgGluArgValLeuGlyLeuIleArg 144
 Db 232 --GCGCCCTGTTCCATTGGAAAGACGTTAGCCGCCGACAG 270

QY 145 CysGluLeuGinSerIleMetGlyGlyGlyThrGlyGluAlaMetAlaValLeuGlyLeuIleArg 164
 Db 271 -----GAAGCCCTGTCGGCGCTACTGAG 297

QY 165 TriArg 166
 Db 298 TTCCGC 303

RESULT 12
 US-09-252-991A-7804
 ; Sequence 7804, Application US/09252991A
 ; General Information:
 ; Patient No. 6551795
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/094,190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 7804
 ; LENGTH: 702
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-7804

Alignment Scores:
 Pred. No.: 0.193
 Score: 112.50
 Percent Similarity: 41.62%
 Best Local Similarity: 26.40%
 Length: 702
 Matches: 52
 Conservative: 30
 Mismatches: 84

PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 8799
; LENGTH: 906
; TYPE: DNA
; ORGANISM: *Pseudomonas aeruginosa*
; US-09-252-991A-3541
Alignment Scores:
Pred. No.: 0.0183 Length: 1074
Score: 131.00 Matches: 54
Percent Similarity: 41.948 Conservative: 24
Best Local Similarity: 29.038 Mismatches: 60
Query Match: 10.468 Indels: 48
DB: 1 Gaps: 8
US-09-252-991A-26292 (1-245) x US-09-252-991A-3541 (1-1074)
Y 63 AlaArgGlyLysLeuLeuGlnThrAlaAlaLisLeuPheArgSerLysGlyLyrGluArg 82
Db 1011 TCCCCGACCGAGCTCTCCACCGCAGCCGACCTTCCGRCGCTACGGCTACACAGGC 952
Qy 83 ThrThrValArgAspIleAspAlaValAlaGlyIleGlnSerGlySerIlePheHis 102
Db 951 ACCACCATGGACATGCTGCTCAGGCCCTGGGCTTGACCAAGGCCCTGTTACACAT 892
Qy 103 PheLysSerLysAspGluIleLeuArgSerValMetGluGluThr--- 117
Db 891 TACCCGAACAGGAGACCTTGCTCCGGCAGCTCTGAAATGACCCACCGGGCTGCC 832
Oy 118 -----IleLeuTyraSerThrAlaLeu----- 124
Db 831 GAGAGCCTCTCAGCATGCCCTACGACCCCCGCTGCTGACGCCCGCGAGCC 772
Qy 125 -----MetArgAlaAlaLeuAlaAspAlaGluAspIleAspIleGluAlaGlyLeu 142
Db 771 CTCGGCGCAGGCCGCCGTTGTCAGGAGCACGACGATGGCTGGCTGGCTGTGGGGTG 712
Qy 143 lle-----ArgCysGluLeu-----GlnSerIleMet 151
Db 711 GTCGCGGTCAAGGCCAGCTATGGTCGCAAGGAGCTGATGGGGCGATCCGGAGCTTC 652
Oy 152 GlyGlyThrGlyGluAlaMetAlaValAlaValAlaValAlaValAlaValAlaLeu 171
Db 651 GACGACTGGCGCAAGCCTTGCCCGCTC 601
Qy 172 GlyGlnAlaIleIleIleGlyLeuArgAspIleIleGlyLeuAlaValAlaValAla 191
Db 600 GCGCAGCGCAGGAGCGCGC 556
Qy 192 GlyGluAlaArgLeuAla-----GlyTyrCysGlnGlyAspProPhe 205
Db 555 GGCGCATCTCGCTGGCGCCATCTATGGCGAGCCGGCTATATCGATGGC 505
Oy 206 IleLeuArgArgPheLeu 211
Db 504 GTCACCCGGGGAGCGCTG 487
RESULT 7
US-09-252-991A-8799
Sequence 8799, Application US/09252991A
; GENERAL INFORMATION:
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; ORGANISM: *Pseudomonas aeruginosa*
; US-09-252-991A-8799
Alignment Scores:
Pred. No.: 0.14 Length: 906
Score: 117.00 Matches: 54
Percent Similarity: 38.46% Conservative: 36
Best Local Similarity: 33.08% Mismatches: 82
Query Match: 9.35% Indels: 62
DB: 1 Gaps: 9
US-09-252-991A-26292 (1-245) x US-09-252-991A-8799 (1-906)
Qy 18 AlaAlaGlyArgAlaAlaAspGluArgHisArgAlaAlaAspAspProGluLysGlyTyrSer 37
Db 20 TCGGTGCGCCGCTCCAGCGAACCGGCAGACGGAGAGACGAAATCACATACGCT 79
Qy 38 AlaLeu----- 39
Db 80 GCGTATGTCACAAATCATGGAGACATACGGACGAGCTGATGTCATTACCTGAGCCCTTC 139
Qy 40 -----AspAspGlnLysAlaArgGluValMetLeuGluLeuValAlaThrGlyGln 56
Db 140 GCCACCCGGAGACCCGGCAGGCCGCCAACCTCCGGCCGAGATGATC----- 187
Qy 57 LeuThrAspProGlySerAlaArgGlyLysSerValMetGluGluGlnThrAlaAlaLisLeuPheArg 76
Db 188 -----GAGGAAACCGCGCCAGTGATGTCACGCCGCCGCCGAGCTTGCC 235
Qy 77 SerLysGlyTyrGluArgThrThrValArgAspIleAlaSerAlaValAlaGlyIleGlnSer 96
Db 236 GACAACGGCTACGCCGCCGCTCGATGAGCCACTGACGCCAGGCCCTCACCGC 295
Qy 97 GlySerIlePheHis1PheLysSerLysAspGluIleLeuArgSerValMetGluGlu 116
Db 296 GGCGGCTGTGATCACACTTGCGGACAAGAAGAGSCTGCTGGCCACGGCTGTGACAGCAG 355
Qy 117 ThrIleLeuTyraSerThrAlaLeuMetArgAlaAlaLeuAlaAspAlaGluAspLeu--- 135
Db 356 ATCGACGACGGAGATGATCTCGCCCTGGCCCATCTGGCTGGCCGAGCACCTGG 415
Qy 136 -----ArgIleArgValLeuIleGlyLeuIleArgCysGluLeuIleGlyLeu 148
Db 416 AGCGCCTCGTGCCTACAACGGGCTACTGGGAATGGCCCTGGAGCGGAATCCAG 475
Qy 149 SerIleMetGlyGlyThrGlyGluAlaMetAlaValAlaLeu-----Val 162
Db 476 CGCATCGTC-----CTGCGCGATGCCCGCCATCTGGCAGCCAGCAGGAGGC 529
Qy 163 TyrGluIlePheArgSerIleSerAla---GluGlyGlnAlaIleIleIleGlyLeuArgAsp 181
Db 530 AGCCAACTGCGCTGCTTAAGCTCGATGACCCGGCA-----CTGGCGGA 574
Qy 182 IleIleGlyLeuGluIleIleIleAspValAlaLeuGlyGluAlaArgLeuAlaGlyTyrCysGln 201
Db 575 CTGATGAGCAGC-----GGCGCGTCCGC-----CGC 601
Qy 202 GlyAspProPheIleLeuArgArgPheLeuThrGlyAlaLeu 215
Db 602 ACCGAGCCGAGGCCCTGGCCGTGCTCAACGGCGCTG 643
RESULT 8
US-09-252-991A-8914
; Sequence 8914, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*

Pred. No.: 0.000958 Length: 732
 Score: 145.00 Matches: 66
 Percent Similarity: 37.65% Conservative: 27
 Best Local Similarity: 26.72% Mismatches: 78
 Query Match: 11.58% Indels: 77
 DB: Gaps: 11 LENGTH: 651

US-09-252-991A-26292 (1-245) x US-09-252-991A-10194 (1-732)

Qy 2 ProthrSerThrCysGlyAlaIleProArgProValGlyLysTyrGlyAlaIleGlyArg 21
 Db 10 CAGACGGCCCTCTGAGGGCTTGCCACCC-.....ACGGGCCT 48

Qy 22 AlaAspGluArgHisArgAlaAlaAspAspProGluLysGlyTyrSerAlaLeuAsp 41
 Db 49 TGC-----CGCAC--GTCGCTGGCCGCGCATTGAGGAGCTCATG----- 93

Qy 42 GlntysAlaArgGluValMetLeuGluLeuValAlaIleThrGlyGlnLeuThrAspProGlu 61
 Db 94 CGCCGCTACCAAGAA-----.....GAAGCCGA 117

Qy 62 serAlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGlu 81
 Db 118 CAGACCCGCTCAAGATCAGATCAGCCGCGCCGCTCCAGCTTGCCGACGGCTATCG 177

Qy 82 ArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHis 101
 Db 178 AACACACCACCTGGCGATGATGCCGAGGCCGCTCAGCCCTGGCCGACGACTCG 237

Qy 102 HisPheIysSerIysAspGluLeuLeuArgSerValMetGluGluThrIleLeuThrAsn 121
 Db 238 CACTCAAGAGCAGAGCAGG-----..... 258

Qy 122 ThrAlaLeuMetArgAlaAlaLeuAlaAspLeuAlaSerGluArgGluArgValLeuGly 141
 Db 259 -----CTGAGAAGAGGGCTGCGCTACTCCAGGACGCCGCTGGAGCTGAGCTATCG 312

Qy 142 LeuIleArgCysGluLeuGlnSerIleMetGlyIleGlyLysLeuPheArgSerLysGlyTyrGlu 161
 Db 313 -----CAAGAGTGCACGTCGCGCTAGGCCGAGCTGCGCTGAGACTTC 360

Qy 162 ValTyRGlutPheArgSerLeuSerAlaGluGlyGlnAlaTyRileLeuGlyLeuArgAsp 181
 Db 361 GTCGCGCAAGTGGTTCGCTGGACGAGGCTGGTATCG-GCACGCTCTCGAGAT 419

Qy 182 IleTyRGlutGlnMetTrpLeuAsp-----..... 189

Db 420 CTGCTGAGAAC-----.....GACCGAACTCACCGCGAGATGCCGAGCCTGAAACG 470

Qy 190 -----ValLeuGlyGluAlaArgLeuAlaGlyTyr 199
 Db 471 CGAACCGCAAGCTCACCGCGCATGGTSCAGTTCGAGGAGCTGAT----- 518

Qy 200 CysGlyGlyAspProHeIleLeuArgGlyPheLeuThrGlyAlaLeuSerThrThr 219
 Db 519 TGCCTAACGGC-----.....GCACCGCGATGAGGATCGGCCGATCACTGGCTTGCT 566

Qy 220 ThrTrpPheArgProGluGly 226
 Db 567 GCTCTATTCGAGGCCCTGATGG 587

RESULT 5
 US-09-252-991A-3553
 ; Sequence 3553, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18
 PRIORITY APPLICATION NUMBER: US 60/094,190
 PRIORITY FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 3553
 LENGTH: 651
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-3553

Alignment Scores:
 Pred. No.: 0.008 Length: 651
 Score: 131.00 Matches: 54
 Percent Similarity: 41.94% Conservative: 24
 Best Local Similarity: 29.03% Mismatches: 60
 Query Match: 10.46% Indels: 48
 DB: Gaps: 8

US-09-252-991A-26292 (1-245) x US-09-252-991A-3553 (1-651)

Qy 63 AlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArg 82
 Db 109 TCCCGCAGGAGCTCTCCAGCGCTGCGCCGGCACCTCCGGCTGCTACGGCTACACCGC 168

Qy 83 ThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHis 102
 Db 169 ACCACATGGACATCTGCTGTCAGCCGCTTCAGGCTGCTACCCAT 228

Qy 103 PheLysSerIysAspGluLeuLeuArgSerValMetGluGluThr-----..... 117
 Db 229 TACCGGACAAGGAGCCTGCTCGGACGTCCTGGAATGGACCCACCGCGCTCC 288

Qy 118 -----IleTyRGlutAsnThrAlaLeu-----..... 124
 Db 289 GAGACGCCCTCAGCAGTCGCTAGCACCCCTGCTGACGCCCGAGGCCCTGAAAGA 348

Qy 125 -----MetArgAlaAlaLeuAlaAspAlaGluAspLeuArgGluArgValLeuGlyLeu 142
 Db 349 CTCGGCCCAAGGCCGCCGCTGCTGCTGAGACGACGATCGGCTGCTGATGGCGCT 408

Qy 143 Ile-----.....ArgCysGluLeu-----.....GlnSerIleMet 151
 Db 409 GTCCGGTGGACGCCAGCATGGCTGCGACGAGCTGATGCCGCGATCGCAGSTTCG 468

Qy 152 GlyGlyThrGlyGluAlaMetAlaValLeuValTyRGlutPheArgSerLeuSerAlaGlu 171
 Db 469 GACGACTGGCCGCAAGCCTCGCCGAGCT-.....TACCCCCGGCTTGACCAA 519

Qy 172 GlyGlnAlaTyRileLeuGlyLeuArgAspIlePheArgGlyGlnMetTrpLeuAspValLeu 191
 Db 520 GCGCAGGCGCTGGAGCGCGC-----.....CGCACTGGCTGCTGATTCGA 564

Qy 192 GlyGluAlaArgLeuAla-----.....GlyTyrCysGlyGlyAspProPhe 205
 Db 565 GGCSCCATCTGCCTGCGGCCGATCTATGGAGGCTATCGATGGC 615

Qy 206 IleLeuArgArgPheLeu 211
 Db 616 GTACCCGGCGAGCCTG 633

RESULT 6
 US-09-252-991A-3541/C
 ; Sequence 3541, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18

GenCore version 5.1.4_p5-4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2003, 14:50:22 ; Search time 5082 seconds
 (without alignments)
 1.617 Million cell updates/sec

Title: US-09-252-991A-26292
 Perfect score: 1252
 Sequence: 1 MPPSTCGAIPRPGVKGAG. GPMSDLQALEEALAVIKDA 245

Scoring table: BL03UM62
 Xgapext 10.0 ; xgapext 0.5
 Ygapext 10.0 ; ygapext 0.5
 Fgapop 6.0 ; fgapext 7.0
 Delop 6.0 ; delext 7.0

Searched: 16571 seqs, 16774251 residues

Total number of hits satisfying chosen parameters: 33142

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
 -MODEL:frame+p2n.model -DEV=soft -Q=allen991.pep -DB=6551795.seq -SUFFIX=ptc
 -OUT=align_26292 -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1
 -END=1 -MATRIX=bl03um62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR SCORE=PCT -THR MAX=1.00 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTMT=ptc
 -NDR=ext -HEA=SIZE=0 -MAXLEN=0 -MINLEN=0 -NCPUR=5 -NO_XLPRY=1
 -NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPD=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : 6551795.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

RESULT 1
 US-09-252-991A-9721
 ; Sequence 9721; Application US/09252991A
 ; Patent No. 6551795

GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196_136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 9721
 ; LENGTH: 738
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9721

Alignment Scores:
 Pred. No.: 2.87e-83
 Score: 1252.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 1
 Gaps: 0

US-09-252-991A-26292 (1-245) x US-09-252-991A-9721 (1-738)

QY 1 MetProThrSerThrCysGlyAlaIleProArgProValGlyLysTyrGlyAlaAlaGly 20
 Db 1 ATGCCGACAACTGCGGCCATCCGAGGCCGTCGGCAATACGGAGCGGCCGG 60

QY 21 ArgAlaAspGluArgIleArgAlaAlaAspAspProGluLysGlyTyr-SerAlaLeuAsp 40
 Db 61 CGGGGGITGAGGCCGACGCCGAGCAGTCGGAAAGGGTACTCAGGCTGGAC 120

QY 41 AspGlnLysAlaArgIleValMetLeuGluLeuValAlaThrGlyIleLeuThrAsp 60
 Db 121 GATCGAAAGGCCGGAAAGTGTGCTGGAGCTGGCTACCGGACAGCTCACCGATCCG 180

QY 61 GluSerAlaArgGlyLysLeuIleGluGlnThrAlaAlaHisLeuPheArgSerLysGlyTyr 80

